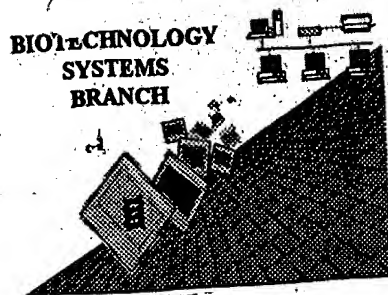


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,737
Source: 01PE
Date Processed by STIC: 6/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
 - 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/873737

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,737

DATE: 06/21/2001

TIME: 17:42:39

Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

pp 1,3-8
Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Duke University
4 Lin, Haifan
W--> 5 <120> TITLE OF INVENTION: PURIFIED AND ISOLATED piwi FAMILY GENES AND GENE
W--> 6 PRODUCTS AND METHODS EMPLOYING SAME
W--> 7 <130> FILE REFERENCE: Attorney Docket No. 180-104 PCT
W--> 8 <140> CURRENT APPLICATION NUMBER:
C--> 9 <141> CURRENT FILING DATE: 2001-06-04
10 <150> PRIOR APPLICATION NUMBER: 60/110,091
11 <151> PRIOR FILING DATE: 1998-12-04
W--> 12 <160> NUMBER OF SEQ ID: 21
13 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

273 <210> SEQ ID NO: 2
274 <211> LENGTH: 843
275 <212> TYPE: PRT
276 <213> ORGANISM: Drosophila sp.
278 <400> SEQUENCE: 2
E--> 279 Met Ala Asp Asp Gln Gly Arg Gly Arg Arg Arg Pro Xaa Asn Glu Asp
280 1 5 10 15
282 Asp Ser Ser Thr Ser Arg Gly Ser Gly Asp Gly Pro Arg Val Lys Val
283 20 25 30
285 Phe Arg Gly Ser Ser Ser Gly Asp Pro Arg Ala Asp Pro Arg Ile Glu
286 35 40 45
288 Ala Ser Arg Glu Arg Arg Ala Leu Glu Glu Ala Pro Arg Arg Glu Gly
289 50 55 60
291 Gly Pro Pro Glu Arg Lys Pro Trp Gly Asp Gln Tyr Asp Tyr Leu Asn
292 65 70 75 80
294 Thr Arg Pro Val Glu Leu Val Ser Lys Lys Gly Thr Asp Gly Val Pro
295 85 90 95
E--> 297 Val Met Leu Gln Thr Asn Phe Phe Arg Xaa Lys Thr Lys Pro Glu Trp
298 100 105 110
300 Arg Ile Val His Tyr His Val Glu Phe Val Pro Thr Ile Glu Asn Pro
301 115 120 125
303 Arg Val Arg Met Gly Val Leu Ser Asn His Ala Asn Leu Leu Gly Ser
304 130 135 140
306 Gly Tyr Leu Phe Asp Gly Leu Gln Leu Phe Thr Thr Arg Lys Phe Glu
307 145 150 155 160
309 Gln Glu Ile Thr Val Leu Ser Gly Lys Ser Lys Leu Asp Ile Glu Tyr
310 165 170 175
311 Lys Ile Ser Ile Lys Phe Val Gly Phe Ile Ser Cys Ala Glu Pro Arg
312 180 185 190
314 Phe Leu Gln Val Leu Asn Leu Ile Leu Arg Arg Ser Met Lys Gly Leu
315 195 200 205
317 Asn Leu Glu Leu Val Gly Arg Asn Leu Phe Asp Pro Arg Ala Lys Ile

*p. 3, too**see item 9 on Eva**summary
sheet*

RAW SEQUENCE LISTING

DATE: 06/21/2001

PATENT APPLICATION: US/09/873,737

TIME: 17:42:39

Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

```

318      210      215      220
320 Glu Ile Arg Glu Phe Lys Met Glu Leu Trp Pro Gly Tyr Glu Thr Ser
321 225      230      235      240
323 Ile Arg Gln His Glu Lys Asp Ile Leu Leu Gly Thr Glu Ile Thr His
324      245      250      255
326 Lys Val Met Arg Thr Glu Thr Ile Tyr Asp Ile Met Arg Arg Cys Ser
327      260      265      270
329 His Asn Pro Ala Arg His Gln Asp Glu Val Arg Val Asn Val Leu Asp
330      275      280      285
332 Leu Ile Val Leu Thr Asp Tyr Asn Asn Arg Thr Tyr Arg Ile Asn Asp
333      290      295      300
335 Val Asp Phe Gly Gln Thr Pro Lys Ser Thr Phe Ser Cys Lys Gly Arg
336 305      310      315      320
338 Asp Ile Ser Phe Val Glu Tyr Tyr Leu Thr Lys Tyr Asn Ile Arg Ile
339      325      330      335
341 Arg Asp His Asn Gln Pro Leu Leu Ile Ser Lys Asn Arg Asp Lys Ala
342      340      345      350
345 Leu Lys Thr Asn Ala Ser Glu Leu Val Val Leu Ile Pro Glu Leu Cys
346      355      360      365
348 Arg Val Thr Gly Leu Asn Ala Glu Met Arg Ser Asn Phe Gln Leu Met
349      370      375      380
351 Arg Ala Met Ser Ser Tyr Thr Arg Met Asn Pro Lys Gln Arg Thr Asp
352 385      390      395      400
354 Arg Leu Arg Ala Phe Asn His Arg Leu Gln Asn Thr Pro Glu Ser Val
355      405      410      415
357 Lys Val Leu Arg Asp Trp Asn Met Glu Leu Asp Lys Asn Val Thr Glu
358      420      425      430
360 Val Gln Gly Arg Ile Ile Gly Gln Gln Asn Ile Val Phe His Asn Gly
361      435      440      445
363 Lys Val Pro Ala Gly Glu Asn Ala Asp Trp Gln Arg His Phe Arg Asp
364      450      455      460
366 Gln Arg Met Leu Thr Thr Pro Ser Asp Gly Leu Asp Arg Trp Ala Val
367 465      470      475      480
369 Ile Ala Pro Gln Arg Asn Ser His Glu Leu Arg Thr Leu Leu Asp Ser
370      485      490      495
372 Leu Tyr Arg Ala Ala Ser Gly Met Gly Leu Arg Ile Arg Ser Pro Gln
373      500      505      510
375 Glu Phe Ile Ile Tyr Asp Asp Arg Thr Gly Thr Tyr Val Arg Ala Met
376      515      520      525
378 Asp Asp Cys Val Arg Ser Asp Pro Lys Leu Ile Leu Cys Leu Val Pro
379      530      535      540
381 Asn Asp Asn Ala Glu Arg Tyr Ser Ser Ile Lys Lys Arg Gly Tyr Val
382 545      550      555      560
384 Asp Arg Ala Val Pro Thr Gln Val Val Thr Leu Lys Thr Thr Lys Asn
385      565      570      575
387 Arg Ser Leu Met Ser Ile Ala Thr Lys Ile Ala Ile Gln Leu Asn Cys
388      580      585      590
390 Lys Leu Gly Tyr Thr Pro Trp Met Ile Glu Leu Pro Leu Ser Gly Leu
391      595      600      605

```

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PATENT APPLICATION: US/09/873,737

TIME: 17:42:39

Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

```

393 Met Thr Ile Gly Phe Asp Ile Ala Lys Ser Thr Arg Asp Arg Lys Arg
394      610      615      620
396 Ala Tyr Gly Ala Leu Ile Ala Ser Met Asp Leu Gln Gln Asn Ser Thr
397 625      630      635      640
399 Tyr Phe Ser Thr Val Thr Glu Cys Ser Ala Phe Asp Val Leu Ala Asn
400      645      650      655
402 Thr Leu Trp Pro Met Ile Ala Lys Ala Leu Arg Gln Tyr Gln His Glu
403      660      665      670
406 His Arg Lys Leu Pro Ser Arg Ile Val Phe Tyr Arg Asp Gly Val Ser
407      675      680      685
409 Ser Gly Ser Leu Lys Gln Leu Phe Glu Phe Glu Val Lys Asp Ile Ile
410      690      695      700
412 Glu Lys Leu Lys Thr Glu Tyr Ala Arg Val Gln Leu Ser Pro Pro Gln
413 705      710      715      720
415 Leu Ala Tyr Ile Val Val Thr Arg Ser Met Asn Thr Arg Phe Phe Leu
416      725      730      735
418 Asn Gly Gln Asn Pro Pro Pro Gly Thr Ile Val Asp Asp Val Ile Thr
419      740      745      750
421 Leu Pro Glu Arg Tyr Asp Phe Tyr Leu Val Ser Gln Gln Val Arg Gln
422      755      760      765
424 Gly Thr Val Ser Pro Thr Ser Tyr Asn Val Leu Tyr Ser Ser Met Gly
425      770      775      780
E--> 427 Xaa Ser Pro Glu Lys Met Gln Lys Leu Thr Tyr Lys Met Cys His Leu
428 785      790      795      800
430 Tyr Tyr Asn Trp Ser Gly Thr Thr Arg Val Pro Ala Val Cys Gln Tyr
431      805      810      815
433 Ala Lys Lys Leu Ala Thr Leu Val Gly Thr Asn Leu His Ser Ile Pro
434      820      825      830
436 Gln Asn Ala Leu Glu Lys Lys Phe Tyr Tyr Leu
437      835      840
736 <210> SEQ ID NO: 4
737 <211> LENGTH: 862
738 <212> TYPE: PRT
739 <213> ORGANISM: Mus sp.
741 <400> SEQUENCE: 4
742 Met Thr Gly Arg Ala Arg Ala Arg Gly Arg Ala Arg Gly Gln
743 1      5      10      15
745 Glu Thr Val Gln His Val Gly Ala Ala Ser Gln Gln Pro Gly Tyr
746      20      25      30
748 Ile Pro Pro Arg Pro Gln Gln Ser Pro Thr Glu Gly Asp Leu Val Gly
749      35      40      45
751 Arg Gly Arg Gln Arg Gly Met Val Val Gly Ala Thr Ser Lys Ser Gln
752      50      55      60
754 Glu Leu Gln Ile Ser Ala Gly Phe Gln Glu Leu Ser Leu Ala Glu Arg
755 65      70      75      80
E--> 757 Gly Gly Arg Arg Arg Asp Phe His Asp Xaa Gly Val Asn Thr Arg Gln
758      85      90      95
760 Asn Leu Asp His Val Lys Glu Ser Lys Thr Gly Ser Ser Gly Ile Ile
761      100      105      110

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item 9

RAW SEQUENCE LISTING

DATE: 06/21/2001

PATENT APPLICATION: US/09/873,737

TIME: 17:42:39

Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

```

763 Val Lys Leu Ser Thr Asn His Phe Arg Leu Thr Ser Arg Pro Gln Trp
764      115      120      125
766 Ala Leu Tyr Gln Tyr His Ile Asp Tyr Asn Pro Leu Met Glu Ala Arg
767      130      135      140
769 Arg Leu Arg Ser Ala Leu Leu Phe Gln His Glu Asp Leu Ile Gly Arg
770 145      150      155      160
772 Cys His Ala Phe Asp Gly Thr Ile Leu Phe Leu Pro Lys Arg Leu Gln
773      165      170      175
775 His Lys Val Thr Glu Val Phe Ser Gln Thr Arg Asn Gly Glu His Val
776      180      185      190
778 Arg Ile Thr Ile Thr Leu Thr Asn Glu Leu Pro Pro Thr Ser Pro Thr
779      195      200      205
E--> 781 Cys Leu Gln Phe Tyr Asn Ile Xaa Phe Arg Arg Leu Leu Lys Ile Met
782      210      215      220
784 Asn Leu Gln Gln Ile Gly Arg Asn Tyr Tyr Asn Pro Ser Asp Pro Ile
785 225      230      235      240
787 Asp Ile Pro Asn His Arg Leu Val Ile Trp Pro Gly Phe Thr Thr Ser
788      245      250      255
790 Ile Leu Gln Tyr Glu Asn Asn Ile Met Leu Cys Thr Asp Val Ser His
791      260      265      270
793 Lys Val Leu Arg Ser Glu Thr Val Leu Asp Phe Met Phe Asn Leu Tyr
794      275      280      285
796 Gln Gln Thr Glu Glu His Lys Phe Gln Glu Gln Val Ser Lys Glu Leu
797      290      295      300
799 Ile Gly Leu Ile Val Leu Thr Lys Tyr Asn Asn Lys Thr Tyr Arg Val
800 305      310      315      320
802 Asp Asp Ile Asp Trp Asp Gln Asn Pro Lys Ser Thr Phe Lys Lys Ala
803      325      330      335
805 Asp Gly Ser Glu Val Ser Phe Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn
806      340      345      350
808 Gln Glu Ile Thr Asp Leu Lys Gln Pro Val Leu Val Ser Gln Pro Lys
809      355      360      365
E--> 811 Arg Arg Arg Gly Pro Gly Gly Thr Leu Pro Gly Pro Ala Met Xaa Ile
812      370      375      380
814 Pro Glu Leu Cys Tyr Leu Thr Gly Leu Thr Asp Lys Met Arg Asn Asp
815 385      390      395      400
817 Phe Asn Val Met Lys Asp Leu Ala Val His Thr Arg Leu Thr Pro Glu
818      405      410      415
820 Gln Arg Gln Arg Glu Val Gly Arg Leu Ile Asp Tyr Ile His Lys Asp
821      420      425      430
823 Asp Asn Val Gln Arg Glu Leu Arg Asp Trp Gly Leu Ser Phe Asp Ser
824      435      440      445
826 Asn Leu Leu Ser Phe Ser Gly Arg Ile Leu Gln Ser Glu Lys Ile His
827      450      455      460
829 Gln Gly Gly Lys Thr Phe Asp Tyr Asn Pro Gln Phe Ala Asp Trp Ser
830 465      470      475      480
832 Lys Glu Thr Arg Gly Ala Pro Leu Ile Ser Val Lys Pro Leu Asp Asn
833      485      490      495
835 Trp Leu Leu Ile Tyr Thr Arg Arg Asn Tyr Glu Ala Ala Asn Ser Leu

```

item 9

item 9

RAW SEQUENCE LISTING

DATE: 06/21/2001

PATENT APPLICATION: US/09/873,737

TIME: 17:42:39

Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

```

836          500          505          510
838 Ile Gln Asn Leu Phe Lys Val Thr Pro Ala Met Gly Ile Gln Met Lys
839          515          520          525
841 Lys Ala Ile Met Ile Glu Val Asp Asp Arg Thr Glu Ala Tyr Leu Arg
842          530          535          540
844 Ala Leu Gln Gln Lys Val Thr Ser Asp Thr Gln Ile Val Val Cys Leu
845 545          550          555          560
847 Leu Ser Ser Asn Arg Lys Asp Lys Tyr Asp Ala Ile Lys Lys Tyr Leu
848          565          570          575
850 Cys Thr Asp Cys Pro Thr Pro Ser Gln Cys Val Val Ala Arg Thr Leu
851          580          585          590
853 Gly Lys Gln Gln Thr Val Met Ala Ile Ala Thr Lys Ile Ala Leu Gln
854          595          600          605
856 Met Asn Cys Lys Met Gly Gly Glu Leu Trp Arg Val Asp Met Ala Leu
857          610          615          620
859 Lys Leu Ala Met Ile Val Gly Ile Asp Cys Tyr His Asp Thr Thr Ala
860 625          630          635          640
862 Gly Arg Arg Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met
863          645          650          655
865 Thr Arg Trp Phe Ser Arg Cys Val Phe Gln Asp Arg Gly Gln Glu Leu
866          660          665          670
868 Val Asp Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Ser
869          675          680          685
871 Gly Cys Asn Glu Tyr Met Pro Ser Arg Val Ile Val Tyr Arg Asp Gly
872          690          695          700
874 Val Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln
875 705          710          715          720
878 Phe Leu Asp Cys Leu Lys Ser Val Gly Arg Gly Tyr Asn Pro Arg Leu
879          725          730          735
881 Thr Val Ile Val Val Lys Lys Arg Val Asn Ala Arg Phe Phe Ala Gln
882          740          745          750
884 Ser Gly Gly Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val
885          755          760          765
887 Glu Val Thr Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala
888          770          775          780
890 Val Arg Ser Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp
891 785          790          795          800
E--> 893 Ser Ser Gly Leu Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Xaa 800
894          805          810          815 den 9
896 Cys His Val Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro
897          820          825          830
899 Cys Gln Tyr Ala His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His
900          835          840          845
902 Arg Glu Pro Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu
903          850          855          860
1183 <210> SEQ ID NO: 6
1184 <211> LENGTH: 861
1185 <212> TYPE: PRT
1186 <213> ORGANISM: Homo sapiens

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pp 6-7

RAW SEQUENCE LISTING

DATE: 06/21/2001

PATENT APPLICATION: US/09/873,737

TIME: 17:42:39

Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

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1188 <400> SEQUENCE: 6
1189 Met Thr Gly Arg Ala Arg Ala Arg Ala Arg Gly Arg Ala Arg Gly Gln
1190   1           5           10           15
1192 Glu Thr Ala Gln Leu Val Gly Ser Thr Ala Ser Gln Gln Pro Gly Tyr
1193           20           25           30
1195 Ile Gln Pro Arg Pro Gln Pro Pro Pro Ala Glu Gly Glu Leu Phe Gly
1196           35           40           45
1198 Arg Gly Arg Gln Arg Gly Thr Ala Gly Gly Thr Ala Lys Ser Gln Gly
1199           50           55           60
E--> 1201 Leu Gln Ile Ser Ala Gly Phe Gln Glu Leu Ser Xaa Ala Glu Arg Gly
1202   65           70           75           80
1204 Gly Arg Arg Arg Asp Phe His Asp Leu Gly Val Asn Thr Arg Gln Asn
1205           85           90           95
1207 Leu Asp His Val Lys Glu Ser Lys Thr Gly Ser Ser Gly Ile Ile Val
1208           100          105          110
1210 Arg Leu Ser Thr Asn His Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala
1211           115          120          125
1213 Leu Tyr Gln Tyr His Ile Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg
1214           130          135          140
1216 Leu Arg Ser Ala Leu Leu Phe Gln His Glu Asp Leu Ile Gly Lys Cys
1217   145          150          155          160
1219 His Ala Phe Asp Gly Thr Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln
1220           165          170          175
1222 Lys Val Thr Glu Val Phe Ser Lys Thr Arg Asn Gly Glu Asp Val Arg
1223           180          185          190
1225 Ile Thr Ile Thr Leu Thr Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys
1226           195          200          205
1228 Leu Gln Phe Tyr Asn Ile Ile Phe Arg Arg Leu Leu Lys Ile Met Asn
1229           210          215          220
1231 Leu Gln Gln Ile Gly Arg Asn Tyr Tyr Asn Pro Asn Asp Pro Ile Asp
1232   225          230          235          240
1234 Ile Pro Ser His Arg Leu Val Ile Trp Pro Gly Phe Thr Thr Ser Ile
1235           245          250          255
1237 Leu Gln Tyr Glu Asn Ser Ile Met Leu Cys Thr Asp Val Ser His Lys
1238           260          265          270
1240 Val Leu Arg Ser Glu Thr Val Leu Asp Phe Met Phe Asn Phe Tyr His
1241           275          280          285
E--> 1243 Gln Thr Glu Glu His Lys Phe Gln Glu Gln Val Ser Lys Glu Xaa Ile
1244           290          295          300
1246 Gly Leu Val Val Leu Thr Lys Tyr Asn Ile Lys Thr Tyr Arg Val Asp
1247   305          310          315          320
1249 Asp Ile Asp Trp Asp Gln Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp
1250           325          330          335
1252 Gly Ser Gly Val Ser Phe Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln
1253           340          345          350
1255 Glu Ile Thr Asp Leu Lys Gln Pro Val Leu Val Ser Gln Pro Lys Arg
1256           355          360          365
1258 Arg Arg Gly Pro Gly Gly Thr Leu Pro Gly Pro Ala Met Leu Ile Pro
1259           370          375          380

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RAW SEQUENCE LISTING

DATE: 06/21/2001

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Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

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1261 Glu Leu Cys Tyr Leu Thr Gly Leu Thr Asp Lys Met Arg Asn Asp Phe
1262 385                      390                      395                      400
1264 Asn Val Met Lys Asp Leu Ala Val His Thr Arg Leu Thr Pro Glu Gln
1265                      405                      410                      415
1267 Arg Gln Arg Glu Val Gly Arg Leu Ile Asp Tyr Ile His Lys Asn Asp
1268                      420                      425                      430
1270 Asn Val Gln Arg Glu Leu Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn
1271                      435                      440                      445
1273 Leu Leu Ser Phe Ser Gly Arg Ile Leu Gln Thr Glu Lys Ile His Gln
1274                      450                      455                      460
1276 Gly Gly Lys Thr Phe Asp Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys
1277 465                      470                      475                      480
1279 Glu Thr Arg Gly Ala Pro Leu Ile Ser Val Lys Pro Leu Asp Asn Trp
1280                      485                      490                      495
1282 Leu Leu Ile Tyr Thr Arg Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile
1283                      500                      505                      510
1285 Gln Asn Leu Phe Lys Val Thr Pro Ala Met Gly Met Gln Met Arg Lys
1286                      515                      520                      525
1289 Ala Ile Met Ile Glu Val Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val
1290                      530                      535                      540
1292 Leu Gln Gln Lys Val Thr Ala Asp Thr Gln Ile Val Val Cys Leu Leu
1293 545                      550                      555                      560
1295 Ser Ser Asn Arg Lys Asp Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys
1296                      565                      570                      575
1298 Thr Asp Cys Pro Thr Pro Ser Gln Cys Val Val Ala Arg Thr Leu Gly
1299                      580                      585                      590
1301 Lys Gln Gln Thr Val Met Ala Ile Ala Thr Lys Ile Ala Leu Gln Met
1302                      595                      600                      605
1304 Asn Cys Lys Met Gly Gly Glu Leu Trp Arg Val Asp Ile Pro Leu Lys
1305                      610                      615                      620
1307 Leu Val Met Ile Val Gly Ile Asp Cys Tyr His Asp Met Thr Ala Gly
1308 625                      630                      635                      640
1310 Arg Arg Ser Ile Ala Gly Phe Val Ala Ser Ile Asn Glu Gly Met Thr
1311                      645                      650                      655
1313 Arg Trp Phe Ser Arg Cys Ile Phe Gln Asp Arg Gly Gln Glu Leu Val
1314                      660                      665                      670
1316 Asp Gly Leu Lys Val Cys Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser
1317                      675                      680                      685
1319 Cys Asn Glu Tyr Met Pro Ser Arg Ile Ile Val Tyr Arg Asp Gly Val
1320                      690                      695                      700
1322 Gly Asp Gly Gln Leu Lys Thr Leu Val Asn Tyr Glu Val Pro Gln Phe
1323 705                      710                      715                      720
E--> 1325 Leu Asp Cys Leu Lys Ser Ile Gly Arg Gly Tyr Asn Pro Arg (Xaa) Thr
1326                      725                      730                      735
1328 Val Ile Val Val Lys Lys Arg Val Asn Thr Arg Phe Phe Ala Gln Ser
1329                      740                      745                      750
1331 Gly Gly Arg Leu Gln Asn Pro Leu Pro Gly Thr Val Ile Asp Val Glu
1332                      755                      760                      765
1334 Val Thr Arg Pro Glu Trp Tyr Asp Phe Phe Ile Val Ser Gln Ala Val

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Item 9

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,737

DATE: 06/21/2001

TIME: 17:42:39

Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

```

1335      770      775      780
1337 Arg Ser Gly Ser Val Ser Pro Thr His Tyr Asn Val Ile Tyr Asp Asn
1338 785      790      795      800
1340 Ser Gly Leu Lys Pro Asp His Ile Gln Arg Leu Thr Tyr Lys Leu Cys
1341      805      810      815
1343 His Ile Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys
1344      820      825      830
1346 Gln Tyr Ala His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg
1347      835      840      845
1350 Glu Pro Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu
1351      850      855      860

```

1525 <210> SEQ ID NO: 21

1526 <211> LENGTH: 4

1527 <212> TYPE: PRT

1528 <213> ORGANISM: Artificial Sequence

OK-> 1529 <220> FEATURE:

1530 <223> OTHER INFORMATION: Description of Artificial Sequence: linker peptide

1532 <400> SEQUENCE: 21

1533 PPRQ

E--> 1539 -1-

delete
at end of
file

invalid - Per sequence rules (1.822),
use three-letter amino acids
only, and number them under
every 5 amino acids.

FYE

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 06/21/2001

PATENT APPLICATION: US/09/873,737

TIME: 17:42:40

Input Set : A:\180-104.ST25.txt

Output Set: N:\CRF3\06212001\I873737.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:283 W: Missing Blank Line separator, <140> field identifier
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12 M:283 W: Missing Blank Line separator, <160> field identifier
L:19 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:279 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
M:340 Repeated in SeqNo=2
L:444 M:283 W: Missing Blank Line separator, <220> field identifier
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:757 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:910 M:283 W: Missing Blank Line separator, <220> field identifier
L:954 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1201 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:1358 M:283 W: Missing Blank Line separator, <220> field identifier
L:1370 M:283 W: Missing Blank Line separator, <220> field identifier
L:1382 M:283 W: Missing Blank Line separator, <220> field identifier
L:1394 M:283 W: Missing Blank Line separator, <220> field identifier
L:1406 M:283 W: Missing Blank Line separator, <220> field identifier
L:1419 M:283 W: Missing Blank Line separator, <220> field identifier
L:1432 M:283 W: Missing Blank Line separator, <220> field identifier
L:1445 M:283 W: Missing Blank Line separator, <220> field identifier
L:1457 M:283 W: Missing Blank Line separator, <220> field identifier
L:1469 M:283 W: Missing Blank Line separator, <220> field identifier
L:1482 M:283 W: Missing Blank Line separator, <220> field identifier
L:1494 M:283 W: Missing Blank Line separator, <220> field identifier
L:1506 M:283 W: Missing Blank Line separator, <220> field identifier
L:1518 M:283 W: Missing Blank Line separator, <220> field identifier

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L:1529 M:283 W: Missing Blank Line separator, <220> field identifier
L:1539 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:1539 M:252 E: No. of Seq. differs, <211>LENGTH:Input:4 Found:0 SEQ:21